

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



1642  
MAY 31 2002  
01/29/2000

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/428,082A  
Source: 1642  
Date Processed by STIC: 5/28/2002

PT#16

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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TECH CENTER 1600/2500

1642

## RAW SEQUENCE LISTING

DATE: 05/28/2002

PATENT APPLICATION: US/09/428,082A

TIME: 11:56:36

Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

*pp 6-10*  
**Does Not Comply**  
**Corrected Diskette Needed**

*errors*  
*shown on page 10*

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3 <110> APPLICANT: FEIGE, ULRICH
4      LIU, CHUAN-FA
5      CHEETHAM, JANET C.
6      BOONE, THOMAS CHARLES
8 <120> TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
10 <130> FILE REFERENCE: A-527
12 <140> CURRENT APPLICATION NUMBER: 09/428,082A
13 <141> CURRENT FILING DATE: 1999-10-22
15 <150> PRIOR APPLICATION NUMBER: 60/105,371
16 <151> PRIOR FILING DATE: 1998-10-23
18 <160> NUMBER OF SEQ ID NOS: 1127
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 684
24 <212> TYPE: DNA
25 <213> ORGANISM: HUMAN
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(684)
30 <223> OTHER INFORMATION:
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36 1          5          10          15
38 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      96
39 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
40          20          25          30
42 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc      144
43 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
44          35          40          45
46 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag      192
47 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
48          50          55          60
50 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg      240
51 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
52 65          70          75          80
54 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat      288
55 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
56          85          90          95
58 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc      336
59 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
60          100          105          110
62 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag      384

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Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

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63 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
64      115      120      125
66 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
67 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
68      130      135      140
70 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
71 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
72 145      150      155      160
74 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
75 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
76      165      170      175
78 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
79 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
80      180      185      190
82 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
83 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
84      195      200      205
86 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
87 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
88      210      215      220
90 tct ccg ggt aaa      684
91 Ser Pro Gly Lys
92 225
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 228
97 <212> TYPE: PRT
98 <213> ORGANISM: HUMAN
100 <400> SEQUENCE: 2
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103 1      5      10      15
106 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
107      20      25      30
110 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
111      35      40      45
114 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
115      50      55      60
118 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
119 65      70      75      80
122 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
123      85      90      95
126 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
127      100      105      110
130 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
131      115      120      125
134 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
135      130      135      140
138 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
139 145      150      155      160
142 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

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Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

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143          165          170          175
146 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
147          180          185          190
150 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
151          195          200          205
154 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
155          210          215          220
158 Ser Pro Gly Lys
159 225
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163 <211> LENGTH: 18
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: SYNTHETIC SCHEME FOR PREPARATION OF PEGYLATED PEPTIDE
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172 Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala
173 1          5          10          15
176 Arg Ala
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181 <211> LENGTH: 18
182 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: SYNTHETIC SCHEME FOR PREPARATION OF PEGYLATED PEPTIDE
188 <400> SEQUENCE: 4
190 Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala
191 1          5          10          15
194 Arg Ala
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199 <211> LENGTH: 794
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Fc-TMP
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (39)..(779)
209 <223> OTHER INFORMATION:
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213 tctagatttg ttttaactaa ttaaaggagg aataacat atg gac aaa act cac aca      56
214          Met Asp Lys Thr His Thr
215          1          5
217 tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc      104
218 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
219          10          15          20
221 ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct      152
222 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
223          25          30          35

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Input Set : A:\A-527.ST25.txt

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225 gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc      200
226 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
227      40                      45                      50
229 aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca      248
230 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
231 55                      60                      65                      70
233 aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc      296
234 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
235      75                      80                      85
237 ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc      344
238 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
239      90                      95                      100
241 aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc      392
242 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
243      105                      110                      115
245 aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      440
246 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
247      120                      125                      130
249 tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc      488
250 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
251 135                      140                      145                      150
253 aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      536
254 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
255      155                      160                      165
257 cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      584
258 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
259      170                      175                      180
261 ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg      632
262 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
263      185                      190                      195
265 cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac      680
266 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
267      200                      205                      210
269 aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ggt gga      728
270 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly
271 215                      220                      225                      230
273 ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg gct gct cgt      776
274 Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg
275      235                      240                      245
277 gct taatctcgag gatcc      794
278 Ala
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 247
284 <212> TYPE: PRT
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Fc-TMP
290 <400> SEQUENCE: 6
292 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

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Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

```

293 1          5          10          15
296 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
297          20          25          30
300 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
301          35          40          45
304 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305          50          55          60
308 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
309 65          70          75          80
312 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
313          85          90          95
316 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
317          100         105         110
320 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
321          115         120         125
324 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
325          130         135         140
328 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
329 145         150         155         160
332 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
333          165         170         175
336 Pro Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr
337          180         185         190
340 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
341          195         200         205
344 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
345          210         215         220
348 Ser Pro Gly Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg
349 225         230         235         240
352 Gln Trp Leu Ala Ala Arg Ala
353          245
356 <210> SEQ ID NO: 7
357 <211> LENGTH: 861
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial Sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Fc-TMP-TMP
364 <220> FEATURE:
365 <221> NAME/KEY: CDS
366 <222> LOCATION: (39)..(842)
367 <223> OTHER INFORMATION:
370 <400> SEQUENCE: 7
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372                               Met Asp Lys Thr His Thr
373                               1          5
375 tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc      104
376 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
377          10          15          20
379 ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct      152

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/428,082A

DATE: 05/28/2002  
TIME: 11:56:37

Input Set : A:\A-527.ST25.txt  
Output Set: N:\CRF3\05282002\I428082A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 6,7,8  
Seq#:45; Xaa Pos. 8,9,10  
Seq#:56; Xaa Pos. 8,9  
Seq#:57; Xaa Pos. 8,9,10  
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Seq#:60; Xaa Pos. 8,9,10,11,12,13  
Seq#:71; Xaa Pos. 2,12  
Seq#:72; Xaa Pos. 2,3,13  
Seq#:73; Xaa Pos. 2,12,13  
Seq#:74; Xaa Pos. 2,3,13,14  
Seq#:83; Xaa Pos. 2,4,5,8,11,13  
Seq#:84; Xaa Pos. 2,4,5,8,11,13,16,18,19,22,25,27  
Seq#:85; Xaa Pos. 2,4,5,8,11,13  
Seq#:86; Xaa Pos. 2,4,5,8,11,13  
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Seq#:102; Xaa Pos. 1,4  
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Seq#:212; Xaa Pos. 1,2,3,5,7,8,9  
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Seq#:246; Xaa Pos. 10  
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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/428,082ADATE: 05/28/2002  
TIME: 11:56:37Input Set : A:\A-527.ST25.txt  
Output Set: N:\CRF3\05282002\I428082A.raw

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RAW SEQUENCE LISTING ERROR SUMMARY  
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DATE: 05/28/2002  
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Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

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Seq#:645; Xaa Pos. 1  
Seq#:765; Xaa Pos. 12,13,16  
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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/428,082ADATE: 05/28/2002  
TIME: 11:56:37

Input Set : A:\A-527.ST25.txt

Output Set: N:\CRF3\05282002\I428082A.raw

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Seq#:937; Xaa Pos. 10  
Seq#:938; Xaa Pos. 10  
Seq#:939; Xaa Pos. 10  
Seq#:940; Xaa Pos. 5,10  
Seq#:941; Xaa Pos. 5,10  
Seq#:942; Xaa Pos. 6,10  
Seq#:943; Xaa Pos. 6,10  
Seq#:944; Xaa Pos. 5,10  
Seq#:945; Xaa Pos. 10  
Seq#:946; Xaa Pos. 10  
Seq#:947; Xaa Pos. 10  
Seq#:948; Xaa Pos. 10  
Seq#:949; Xaa Pos. 10  
Seq#:950; Xaa Pos. 1,10  
Seq#:951; Xaa Pos. 10  
Seq#:952; Xaa Pos. 10  
Seq#:953; Xaa Pos. 10  
Seq#:954; Xaa Pos. 10  
Seq#:955; Xaa Pos. 10  
Seq#:956; Xaa Pos. 5  
Seq#:957; Xaa Pos. 5  
Seq#:958; Xaa Pos. 5  
Seq#:959; Xaa Pos. 5  
Seq#:961; Xaa Pos. 3  
Seq#:962; Xaa Pos. 7  
Seq#:963; Xaa Pos. 10,11  
Seq#:964; Xaa Pos. 1,10,11  
Seq#:965; Xaa Pos. 8,10  
Seq#:966; Xaa Pos. 8,10  
Seq#:967; Xaa Pos. 7,10  
Seq#:968; Xaa Pos. 7,10  
Seq#:969; Xaa Pos. 3,10  
Seq#:970; Xaa Pos. 3,10  
Seq#:971; Xaa Pos. 1,10  
Seq#:972; Xaa Pos. 1,10  
Seq#:975; Xaa Pos. 5  
Seq#:979; Xaa Pos. 1,3,4,5,6,7,8,9,10,11  
Seq#:1002; Xaa Pos. 1,2,3,6  
Seq#:1004; Xaa Pos. 10  
Seq#:1006; Xaa Pos. 10  
Seq#:1007; Xaa Pos. 10  
Seq#:1008; Xaa Pos. 10  
Seq#:1009; Xaa Pos. 10  
Seq#:1010; Xaa Pos. 10  
Seq#:1011; Xaa Pos. 10

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/428,082A

DATE: 05/28/2002  
TIME: 11:56:37

Input Set : A:\A-527.ST25.txt  
Output Set: N:\CRF3\05282002\I428082A.raw

Seq#:1012; Xaa Pos. 10  
Seq#:1013; Xaa Pos. 10  
Seq#:1014; Xaa Pos. 10  
Seq#:1015; Xaa Pos. 10  
Seq#:1016; Xaa Pos. 10  
Seq#:1018; Xaa Pos. 10  
Seq#:1019; Xaa Pos. 10  
Seq#:1020; Xaa Pos. 10  
Seq#:1021; Xaa Pos. 10  
Seq#:1022; Xaa Pos. 10  
Seq#:1023; Xaa Pos. 10  
Seq#:1042; Xaa Pos. 1,2,3,4,7,10,11  
Seq#:1043; Xaa Pos. 3,4  
Seq#:1091; Xaa Pos. 6  
Seq#:1092; Xaa Pos. 2,3,8,9  
Seq#:1093; Xaa Pos. 2,4

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:215,260,556,652,683,741,762,897,961,964,977,983

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"  
or "Unknown". Please explain source of genetic material in <220> to <223>  
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
(Sec.1.823 of new Rules)

Seq#:215,556,652,683,741,762,977,983

*The errors in the submitted file*